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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/847,392

DATE: 12/17/2001

TIME: 12:05:26

Input Set : N:\Cr3\RULE60\09847392.txt

Output Set: N:\CRF3\12172001\I847392.raw

3 <110> APPLICANT: LIVSHITS, VITALY ARKADIEVICH
4 ZAKATAEVA, NATALYA PAVLOVNA
5 ALCOSHIN, VLADIMIR VENYAMIOVICH
6 BELAREOVA, ALL VALENTINOVNA
7 TOKHMAKOVA, IRINA LVOVNA
9 <120> TITLE OF INVENTION: DNA CODING FOR PROTEIN WHICH CONFERS ON BACTERIUM
10 ESCHERICHIA COLI RESISTANCE TO L0-HOMOSERINE AND METHOD
11 FOR PRODUCING L-AMINO ACIDS
13 <130> FILE REFERENCE: 0010-1039-0
15 <140> CURRENT APPLICATION NUMBER: 09/847,392
16 <141> CURRENT FILING DATE: 2001-05-03
18 <150> PRIOR APPLICATION NUMBER: 09/396,357
19 <151> PRIOR FILING DATE: 1999-09-15
21 <150> PRIOR APPLICATION NUMBER: RU98118425
22 <151> PRIOR FILING DATE: 1998-10-13
24 <160> NUMBER OF SEQ ID NOS: 2
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1200
30 <212> TYPE: DNA
31 <213> ORGANISM: Escherichia coli
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (557)..(1171)
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42 cgattaacat gcccgagatg cggatcggct aacaggcgac cggaacgtcc ctgccgcga 180
44 tggctgatga ttaagacatc aaaccccaaa tggaacaggt cataggccag ttccgcatat 240
46 tttagctagc tctcaatacg ccccgggcag atgactacca cccggtcatg gtgctgtgcg 300
48 cgaaaacgga caaagcgcac cggaatgtca tccacaccag taaactctgc ttcacacgc 360
50 tgacgccaga aatcagtcag cgggtcccatg gtaaaagcag caaacgcgtt ttctcttgtt 420
52 tcccagtcct tttgtgtgctg aaacatcggg taatctgcct cttaaacacac gtaaaatcgt 480
54 tttttttagc gtgcctgaca caacgctgcg acagtagcgt attgtggcac aaaaatagac 540
56 acaccgggag ttcacat atg acc tta gaa tgg tgg ttt gcc tac ctg ctg aca 592
57 Met Thr Leu Glu Trp Trp Phe Ala Tyr Leu Leu Thr
58 1 5 10
60 tcg atc att tta acg ctg tgc cca ggc tct ggt gca atc aac act atg 640
61 Ser Ile Ile Leu Thr Leu Ser Pro Gly Ser Gly Ala Ile Asn Thr Met
62 15 20 25
64 acc acc tgc ctc aac cac ggt tat ccg gcc ggt ggc gtc tat tgc tgg 688
65 Thr Thr Ser Leu Asn His Gly Tyr Pro Ala Gly Gly Val Tyr Cys Trp
66 30 35 40
68 gct tca gac cgg act ggc gat tca tat tgt gct ggt tgg cgt ggg gtt 736
69 Ala Ser Asp Arg Thr Gly Asp Ser Tyr Cys Ala Gly Trp Arg Gly Val
70 45 50 55 60
72 ggg acg cta ttt tcc cgc tca gtg att gcg ttt gaa gtg ttg aag tgg 784

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73 Gly Thr Leu Phe Ser Arg Ser Val Ile Ala Phe Glu Val Leu Lys Trp
74          65          70          75
76 gca ggc gcg gct tac ttg att tgg ctg gga atc cag cag tgg cgc gcc      832
77 Ala Gly Ala Ala Tyr Leu Ile Trp Leu Gly Ile Gln Gln Trp Arg Ala
78          80          85          90
80 gct ggt gca att gac ctt aaa tcg ctg gcc tct act caa tcg cgt cga      880
81 Ala Gly Ala Ile Asp Leu Lys Ser Leu Ala Ser Thr Gln Ser Arg Arg
82          95          100          105
84 cat ttg ttc cag cgc gca gtt ttt gtg aat ctc acc aat ccc aaa agt      928
85 His Leu Phe Gln Arg Ala Val Phe Val Asn Leu Thr Asn Pro Lys Ser
86          110          115          120
88 att gtg ttt ctg gcg gcg cta ttt ccg caa ttc atc atg ccg caa cag      976
89 Ile Val Phe Leu Ala Ala Leu Phe Pro Gln Phe Ile Met Pro Gln Gln
90 125          130          135          140
92 ccg caa ctg atg cag tat atc gtg ctc ggc gtc acc act att gtg gtc      1024
93 Pro Gln Leu Met Gln Tyr Ile Val Leu Gly Val Thr Thr Ile Val Val
94          145          150          155
96 gat att att gtg atg atc ggt tac gcc acc ctt gct caa cgg att gct      1072
97 Asp Ile Ile Val Met Ile Gly Tyr Ala Thr Leu Ala Gln Arg Ile Ala
98          160          165          170
100 cta tgg att aaa gga cca aag cag atg aag gcg ctg aat aag att ttc      1120
101 Leu Trp Ile Lys Gly Pro Lys Gln Met Lys Ala Leu Asn Lys Ile Phe
102          175          180          185
104 ggc tcg ttg ttt atg ctg gtg gga gcg ctg tta gca tcg gcg agg cat      1168
105 Gly Ser Leu Phe Met Leu Val Gly Ala Leu Leu Ala Ser Ala Arg His
106          190          195          200
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109 Ala
110 205
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114 <211> LENGTH: 205
115 <212> TYPE: PRT
116 <213> ORGANISM: Escherichia coli
118 <400> SEQUENCE: 2
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122 Thr Leu Ser Pro Gly Ser Gly Ala Ile Asn Thr Met Thr Thr Ser Leu
123          20          25          30
125 Asn His Gly Tyr Pro Ala Gly Gly Val Tyr Cys Trp Ala Ser Asp Arg
126          35          40          45
128 Thr Gly Asp Ser Tyr Cys Ala Gly Trp Arg Gly Val Gly Thr Leu Phe
129          50          55          60
131 Ser Arg Ser Val Ile Ala Phe Glu Val Leu Lys Trp Ala Gly Ala Ala
132 65          70          75          80
134 Tyr Leu Ile Trp Leu Gly Ile Gln Gln Trp Arg Ala Ala Gly Ala Ile
135          85          90          95
137 Asp Leu Lys Ser Leu Ala Ser Thr Gln Ser Arg Arg His Leu Phe Gln
138          100          105          110
140 Arg Ala Val Phe Val Asn Leu Thr Asn Pro Lys Ser Ile Val Phe Leu

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141	115	120	125
143	Ala Ala Leu Phe Pro Gln Phe Ile Met Pro Gln Gln Pro Gln Leu Met		
144	130	135	140
146	Gln Tyr Ile Val Leu Gly Val Thr Thr Ile Val Val Asp Ile Ile Val		
147	145	150	155
149	Met Ile Gly Tyr Ala Thr Leu Ala Gln Arg Ile Ala Leu Trp Ile Lys		
150	165	170	175
152	Gly Pro Lys Gln Met Lys Ala Leu Asn Lys Ile Phe Gly Ser Leu Phe		
153	180	185	190
155	Met Leu Val Gly Ala Leu Leu Ala Ser Ala Arg His Ala		
156	195	200	205

VERIFICATION SUMMARY

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